

OIPE

FHL

## RAW SEQUENCE LISTING

DATE: 07/07/2001

PATENT APPLICATION: US/09/886,856

TIME: 13:08:58

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07062001\I886856.raw

4 <110> APPLICANT: Whitehouse, Martha Jo  
 6 <120> TITLE OF INVENTION: Methods and Compositions for the  
 7 , Treatment of Peripheral Artery Disease  
 10 <130> FILE REFERENCE: PP16090.004  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/886,856  
 C--> 12 <141> CURRENT FILING DATE: 2001-06-21  
 12 <150> PRIOR APPLICATION NUMBER: 60/213,504  
 13 <151> PRIOR FILING DATE: 2000-06-22  
 15 <150> PRIOR APPLICATION NUMBER: 60/264,572  
 16 <151> PRIOR FILING DATE: 2000-01-26  
 18 <150> PRIOR APPLICATION NUMBER: 60/276,549  
 19 <151> PRIOR FILING DATE: 2001-03-16  
 21 <160> NUMBER OF SEQ ID NOS: 9  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 441  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Bos taurus  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (1)...(441)  
 34 <400> SEQUENCE: 1

35	cca gcc cta cca gaa gat ggg ggg tcc ggg gcc ttc cca cca ggg cac	48
36	Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His	
37	1 5 10 15	
39	ttc aaa gat cca aaa cga cta tat tgt aaa aac ggg ggg ttc ttc cta	96
40	Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu	
41	20 25 30	
43	cga atc cac cca gat ggg cga gta gat ggg gta cga gaa aaa tcc gat	144
44	Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp	
45	35 40 45	
47	cca cac atc aaa cta caa cta caa gcc gaa gaa cga ggg gta gta tcc	192
48	Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser	
49	50 55 60	
51	atc aaa ggg gta tgt gcc aac cga tat cta gcc atg aaa gaa gat ggg	240
52	Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly	
53	65 70 75 80	
55	cga cta cta gcc tcc aaa tgt gta acc gat gaa tgt ttc ttc ttc gaa	288
56	Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu	
57	85 90 95	
59	cga cta gaa tcc aac aac tat aac acc tat cga tcc cga aaa tat tcc	336
60	Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser	
61	100 105 110	
63	tcc tgg tat gta gcc cta aaa cga acc ggg caa tat aaa cta ggg cca	384
64	Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro	
65	115 120 125	
67	aaa acc ggg cca ggg caa aaa gcc atc cta ttc cta cca atg tcc gcc	432

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68 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
69      130                      135                      140
71 aaa tcc taa
72 Lys Ser *
73 145
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 146
78 <212> TYPE: PRT
79 <213> ORGANISM: Bos taurus
81 <400> SEQUENCE: 2
82 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
83 1      5      10      15
84 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
85      20      25      30
86 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
87      35      40      45
88 Pro His Ile Lys Leu Gln Leu Ala Glu Glu Arg Gly Val Val Ser
89      50      55      60
90 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
91 65      70      75      80
92 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
93      85      90      95
94 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser
95      100     105     110
96 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro
97      115     120     125
98 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
99      130     135     140
100 Lys Ser
101 145
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 441
106 <212> TYPE: DNA
107 <213> ORGANISM: Homo sapiens
109 <220> FEATURE:
110 <221> NAME/KEY: CDS
111 <222> LOCATION: (1)...(441)
113 <400> SEQUENCE: 3
114 ccc gcc ttg ccc gag gat ggc ggc agc ggc gcc ttc ccg ccc ggc cac
115 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
116 1      5      10      15
118 ttc aag gac ccc aag cgg ctg tac tgc aaa aac ggg ggc ttc ttc ctg
119 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
120      20      25      30
122 cgc atc cac ccc gac ggc cga gtt gac ggg gtc cgg gag aag agc gac
123 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
124      35      40      45
126 cct cac atc aag cta caa ctt caa gca gaa gag aga gga gtt gtg tct
127 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser

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128      50      55      60
130 atc aaa gga gtg tgt gct aac cgt tac ctg gct atg aag gaa gat gga      240
131 ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
132 65      70      75      80
134 aga tta ctg gct tct aaa tgt gtt acg gat gag tgt ttc ttt ttt gaa      288
135 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
136      85      90      95
138 cga ttg gaa tct aat aac tac aat act tac cgg tca agg aaa tac acc      336
139 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr
140      100      105      110
142 agt tgg tat gtg gca ctg aaa cga act ggg cag tat aaa ctt gga tcc      384
143 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser
144      115      120      125
146 aaa aca gga cct ggg cag aaa gct ata ctt ttt ctt cca atg tct gct      432
147 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
148      130      135      140
150 aag agc tga      441
151 Lys Ser *
152 145
155 <210> SEQ ID NO: 4
156 <211> LENGTH: 146
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 4
161 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
162 1      5      10      15
163 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
164      20      25      30
165 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
166      35      40      45
167 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
168      50      55      60
169 ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
170 65      70      75      80
171 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
172      85      90      95
173 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr
174      100      105      110
175 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser
176      115      120      125
177 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
178      130      135      140
179 Lys Ser
180 145
183 <210> SEQ ID NO: 5
184 <211> LENGTH: 468
185 <212> TYPE: DNA
186 <213> ORGANISM: Bos taurus
188 <220> FEATURE:

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189 <221> NAME/KEY: CDS
190 <222> LOCATION: (1)...(468)
192 <400> SEQUENCE: 5
193 atg gca gcc ggg agc atc acc acg ctg cca gcc cta cca gaa gat ggg      48
194 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
195 1 5 10 15
197 ggg tcc ggg gcc ttc cca cca ggg cac ttc aaa gat cca aaa cga cta      96
198 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
199 20 25 30
201 tat tgt aaa aac ggg ggg ttc ttc cta cga atc cac cca gat ggg cga      144
202 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
203 35 40 45
205 gta gat ggg gta cga gaa aaa tcc gat cca cac atc aaa cta caa cta      192
206 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
207 50 55 60
209 caa gcc gaa gaa cga ggg gta gta tcc atc aaa ggg gta tgt gcc aac      240
210 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
211 65 70 75 80
213 cga tat cta gcc atg aaa gaa gat ggg cga cta cta gcc tcc aaa tgt      288
214 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
215 85 90 95
217 gta acc gat gaa tgt ttc ttc ttc gaa cga cta gaa tcc aac aac tat      336
218 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
219 100 105 110
221 aac acc tat cga tcc cga aaa tat tcc tcc tgg tat gta gcc cta aaa      384
222 Asn Thr Tyr Arg Ser Arg Lys Tyr Ser Ser Trp Tyr Val Ala Leu Lys
223 115 120 125
225 cga acc ggg caa tat aaa cta ggg cca aaa acc ggg cca ggg caa aaa      432
226 Arg Thr Gly Gln Tyr Lys Leu Gly Pro Lys Thr Gly Pro Gly Gln Lys
227 130 135 140
229 gcc atc cta ttc cta cca atg tcc gcc aaa tcc taa      468
230 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser *
231 145 150 155
234 <210> SEQ ID NO: 6
235 <211> LENGTH: 155
236 <212> TYPE: PRT
237 <213> ORGANISM: Bos taurus
239 <400> SEQUENCE: 6
240 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
241 1 5 10 15
242 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
243 20 25 30
244 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
245 35 40 45
246 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
247 50 55 60
248 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
249 65 70 75 80
250 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys

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```

251                               85                               90                               95
252 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
253                               100                               105                               110
254 Asn Thr Tyr Arg Ser Arg Lys Tyr Ser Ser Trp Tyr Val Ala Leu Lys
255                               115                               120                               125
256 Arg Thr Gly Gln Tyr Lys Leu Gly Pro Lys Thr Gly Pro Gly Gln Lys
257                               130                               135                               140
258 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
259 145                               150                               155
262 <210> SEQ ID NO: 7
263 <211> LENGTH: 474
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (1)...(468)
271 <400> SEQUENCE: 7
272 atg gca gcc ggg agc atc acc acg ctg ccc gcc ttg ccc gag gat ggc 48
273 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
274 1 5 10 15
276 ggc agc ggc gcc ttc ccg ccc ggc cac ttc aag gac ccc aag cgg ctg 96
277 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
278 20 25 30
280 tac tgc aaa aac ggg ggc ttc ttc ctg cgc atc cac ccc gac ggc cga 144
281 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
282 35 40 45
284 gtt gac ggg gtc cgg gag aag agc gac cct cac atc aag cta caa ctt 192
285 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
286 50 55 60
288 caa gca gaa gag aga gga gtt gtg tct atc aaa gga gtg tgt gct aac 240
289 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
290 65 70 75 80
292 cgt tac ctg gct atg aag gaa gat gga aga tta ctg gct tct aaa tgt 288
293 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
294 85 90 95
296 gtt acg gat gag tgt ttc ttt ttt gaa cga ttg gaa tct aat aac tac 336
297 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
298 100 105 110
300 aat act tac cgg tca agg aaa tac acc agt tgg tat gtg gca ctg aaa 384
301 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
302 115 120 125
304 cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct ggg cag aaa 432
305 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
306 130 135 140
308 gct ata ctt ttt ctt cca atg tct gct aag agc tga ttttaa 474
309 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser *
310 145 150 155
313 <210> SEQ ID NO: 8
314 <211> LENGTH: 155

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/886,856

DATE: 07/07/2001

TIME: 13:08:59

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07062001\I886856.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date